

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
- (ii) TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David A. Jackson, Esq.
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Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/666,020
(B) FILING DATE: 19-JUN-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/227,319
(B) FILING DATE: 13-APR-1994
- (viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 1049-1-004 N1
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGATCCG GTGGAACAAG ATGGATTAT

29

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCGTCGACA TGTGCACAAC TCTGACTG

28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGATTATC AAGTGTCAAG TCCAATCTAT GACATCAATT ATTATACATC GGAGCCCTGC 60

CAAAAA 66

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr
1				5				10					15		

Ser	Glu	Pro	Cys	Gln	Lys
				20	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGATTATC AAGTGTC AAG TCCAATCTAT GACATCAATT ATCCATACGA TGTTCAGAT 60
TATGCTTCGG AGCCCTGCCA AAAA 84

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Pro	Tyr
1				5				10					15		
Asp	Val	Pro	Asp	Tyr	Ala	Ser	Glu	Pro	Cys	Gln	Lys				
			20					25							

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCAATTATC CATACGATGT TCCAGATTAT GCTTCGGAGC CCTGCCAAAA A 51

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotides"
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAGGATCCA CCATGGATTA TCAAGTGTCA AGTCCAATCT ATGACATCAA TTATCCATAC 60

GAT 63

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATACGATG TTCCAGATTA TGCT 24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATACG ATGTTCCAGA TTATGCTTCG

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3383 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAAGAGCTG AGACATCCGT TCCCCTACAA GAAACTCTCC CCGGGTGGAA CAAGATGGAT	60
TATCAAGTGT CAAGTCCAAT CTATGACATC AATTATTATA CATCGGAGCC CTGCCAAAAA	120
ATCAATGTGA AGCAAATCGC AGCCCGCCTC CTGCCTCCGC TCTACTCACT GGTGTTTCATC	180
TTTGGTTTTG TGGGCAACAT GCTGGTCATC CTCATCCTGA TAAACTGCAA AAGGCTGAAG	240
AGCATGACTG ACATCTACCT GCTCAACCTG GCCATCTCTG ACCTGTTTTT CCTTCTTACT	300
GTCCCCTTCT GGGCTCACTA TGCTGCCGCC CAGTGGGACT TTGGAAATAC AATGTGTCAA	360
CTCTTGACAG GGCTCTATTT TATAGGCTTC TTCTCTGGAA TCTTCTTCAT CATCCTCCTG	420
ACAAATCGATA GGTACCTGGC TGTGTCCTCAT GCTGTGTTTG CTTTAAAAGC CAGGACGGTC	480
ACCTTTGGGG TGGTGACAAG TGTGATCACT TGGGTGGTGG CTGTGTTTGC GTCTCTCCCA	540
GGAATCATCT TTACCAGATC TCAAAAAGAA GGTCTTCATT ACACCTGCAG CTCTCATTTT	600
CCATACAGTC AGTATCAATT CTGGAAGAAT TTCCAGACAT TAAAGATAGT CATCTTGGGG	660
CTGGTCCTGC CGCTGCTTGT CATGGTCATC TGCTACTCGG GAATCCTAAA AACTCTGCTT	720
CGGTGTGCGA ATGAGAAGAA GAGGCACAGG GCTGTGAGGC TTATCTTCAC CATCATGATT	780
GTTTATTTTC TCTTCTGGGC TCCCTACAAC ATTGTCCTTC TCCTGAACAC CTTCCAGGAA	840
TTCTTTGGCC TGAATAATTG CAGTAGCTCT AACAGGTTGG ACCAAGCTAT GCAGGTGACA	900
GAGACTCTTG GGATGACGCA CTGCTGCATC AACCCCATCA TCTATGCCTT TGTCGGGGAG	960
AAGTTCAGAA ACTACCTCTT AGTCTTCTTC CAAAAGCACA TTGCCAAACG CTTCTGCAAA	1020
TGCTGTTCTA TTTTCCAGCA AGAGGCTCCC GAGCGAGCAA GCTCAGTTA CACCCGATCC	1080
ACTGGGGAGC AGGAAATATC TGTGGGCTTG TGACACGGAC TCAAGTGGGC TGGTGACCCA	1140
GTCAGAGTTG TGCACATGGC TTAGTTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGGA	1200
GAGGTCTTTT TTAAAAGGAA GTTACTGTTA TAGAGGGTCT AAGATTCATC CATTTATTTG	1260

GCATCTGTTT AAAGTAGATT AGATCTTTTA AGCCCATCAA TTATAGAAAG CCAAATCAAA	1320
ATATGTTGAT GAAAAATAGC AACCTTTTTA TCTCCCCTTC ACATGCATCA AGTTATTGAC	1380
AAACTCTCCC TTCACTCCGA AAGTTCCTTA TGTATATTTA AAAGAAAGCC TCAGAGAATT	1440
GCTGATTCTT GAGTTTAGTG ATCTGAACAG AAATACCAAA ATTATTTTCAG AAATGTACAA	1500
CTTTTTACCT AGTACAAGGC AACATATAGG TTGTAAATGT GTTTAAAACA GGTCTTTGTC	1560
TTGCTATGGG GAGAAAAGAC ATGAATATGA TTAGTAAAGA AATGACACTT TTCATGTGTG	1620
ATTTCCCCTC CAAGGTATGG TTAATAAGTT TCACTGACTT AGAACCAGGC GAGAGACTTG	1680
TGGCCTGGGA GAGCTGGGGA AGCTTCTTAA ATGAGAAGGA ATTTGAGTTG GATCATCTAT	1740
TGCTGGCAAA GACAGAAGCC TCACTGCAAG CACTGCATGG GCAAGCTTGG CTGTAGAAGG	1800
AGACAGAGCT GGTGGGAAG ACATGGGGAG GAAGGACAAG GCTAGATCAT GAAGAACCTT	1860
GACGGCATTG CTCCGTCTAA GTCATGAGCT GAGCAGGGAG ATCCTGGTTG GTGTTGCAGA	1920
AGGTTTACTC TGTGGCCAAA GGAGGGTCAG GAAGGATGAG CATTTAGGGC AAGGAGACCA	1980
CCAACAGCCC TCAGGTCAGG GTGAGGATGG CCTCTGCTAA GCTCAAGGCG TGAGGATGGG	2040
AAGGAGGGAG GTATTTCGTAA GGATGGGAAG GAGGGAGGTA TTCGTGCAGC ATATGAGGAT	2100
GCAGAGTCAG CAGAACTGGG GTGGATTGG TTTGGAAGTG AGGGTCAGAG AGGAGTCAGA	2160
GAGAATCCCT AGTCTTCAAG CAGATTGGAG AAACCCCTGA AAAGACATCA AGCACAGAAG	2220
GAGGAGGAGG AGGTTTAGGT CAAGAAGAAG ATGGATTGGT GTAAAAGGAT GGGTCTGGTT	2280
TGCAGAGCTT GAACACAGTC TCACCCAGAC TCCAGGCTGT CTTTCACTGA ATGCTTCTGA	2340
CTTCATAGAT TTCCTTCCCA TCCCAGCTGA AATACTGAGG GGTCTCCAGG AGGAGACTAG	2400
ATTTATGAAT ACACGAGGTA TGAGGTCTAG GAACATACTT CAGCTCACAC ATGAGATCTA	2460
GGTGAGGATT GATTACCTAG TAGTCATTTT ATGGGTTGTT GGGAGGATTC TATGAGGCAA	2520
CCACAGGCAG CATTTAGCAC ATACTACACA TTCAATAAGC ATCAAACCTCT TAGTTACTCA	2580
TTCAGGGATA GCACTGAGCA AAGCATTGAG CAAAGGGGTC CCATATAGGT GAGGGAAGCC	2640
TGAAAAACTA AGATGCTGCC TGCCCAGTGC ACACAAGTGT AGGTATCATT TTCTGCATTT	2700
AACCGTCAAT AGGCAAAGGG GGGAAGGGAC ATATTCATTT GGAAATAAGC TGCCTTGAGC	2760
CTTAAACCC ACAAAGTAC AATTTACCAG CCTCCGTATT TCAGACTGAA TGGGGGTGGG	2820
GGGGGCGCCT TAGGTACTTA TTCCAGATGC CTTCTCCAGA CAAACCAGAA GCAACAGAAA	2880
AAATCGTCTC TCCCTCCCTT TGAAATGAAT ATACCCCTTA GTGTTTGGGT ATATTCATTT	2940


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CAAAGGGAGA GAGAGAGGTT TTTTCTGTT CTTTCTCATA TGATTGTGCA CATACTTGAG      3000
ACTGTTTTGA ATTTGGGGGA TGGCTAAAAC CATCATAGTA CAGGTAAGGT GAGGGAATAG      3060
TAAGTGGTGA GAACTACTCA GGAATGAAG GTGTCAGAAT AATAAGAGGT GCTACTGACT      3120
TTCTCAGCCT CTGAATATGA ACGGTGAGCA TTGTGGCTGT CAGCAGGAAG CAACGAAGGG      3180
AAATGTCTTT CCTTTTGCTC TTAAGTTGTG GAGAGTGCAA CAGTAGCATA GGACCCTACC      3240
CTCTGGGCCA AGTCAAAGAC ATTCTGACAT CTTAGTATTT GCATATTCTT ATGTATGTGA      3300
AAGTTACAAA TTGCTTGAAA GAAATATGC ATCTAATAAA AAACACCTTC TAAAATAAAA      3360
AAAAAAAAAA AAAAAAAAAA AAA                                           3383

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1           5           10           15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20          25          30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35          40          45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50          55          60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65          70          75          80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85          90          95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100         105         110

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Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
 115 120 125
 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
 130 135 140
 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
 145 150 155 160
 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
 165 170 175
 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
 180 185 190
 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
 195 200 205
 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
 210 215 220
 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
 225 230 235 240
 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
 245 250 255
 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
 260 265 270
 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
 275 280 285
 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
 290 295 300
 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
 305 310 315 320
 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
 325 330 335
 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
 340 345 350